Comparison of hom(oe)ologous chromosome segments in the highly polyploid interspecific genome of sugarcane

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Modern sugarcane cultivars (*Saccharum* spp.) present one of the most complex crop genome studied to date, mainly due to a very high degree of polyploidy (2n = 12x = 120), and an interspecific origin from two autopolyploid species, namely *S. officinarum* and *S. spontaneum*.

To investigate the impact of polyploidization on the sugarcane genome organization and more widely on its performance and plasticity, we finely analyzed the structural organization of hom(oe)ologous chromosome segments. Twenty-seven homoeologous BAC clones from three distinct regions, carrying the genes *Adh1* (13 hom(oe)ologous chromosome segments), *PST2a* (10 hom(oe)ologous chromosome segments) and *CAD2* (4 hom(oe)ologous chromosome segments), were identified, sequenced, finely annotated and compared, representing more than 2.5 Mb of sugarcane DNA sequence. A very high gene colinearity, gene structure and sequence conservation (98.1% of average nucleotide sequence identity for the coding sequence, and 93.3% for the aligned part of the introns) was observed among all hom(oe)ologous chromosome segments, confirming preliminary observations. Based on their structure, the homoeologous genes were predicted to be functional and the vast majority of them showed signs of evolving under purifying selection. Colinearity between hom(oe)ologous chromosomes was also extended to many intergenic regions and transposable elements. Divergence between hom(oe)ologous genes and patterns of transposable element insertions are currently being analyzed in order to infer the origin (*S. officinarum vs S. spontaneum*) of the chromosome segments.

The high level of gene colinearity and structure conservation has implication regarding whole genome sequencing strategy of this complex genome, since it suggests that one chromosome segment could serve as reference for the other hom(oe)ologous chromosome segments regarding gene content. The maintenance of a broad set of functional alleles, that we described, may be involved in the high phenotypic plasticity and wide adaptation of sugarcane.